IN THE SPECIFICATION

Please substitute the paragraph at page 3, lines 15-20 with the following replacement paragraph. A marked-up copy of this paragraph, showing the changes made thereto, is attached.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows the construction steps of β1,3-galactosyltransferase plasmids pBBPIJ and pBBPJ.

FIG. 2 shows the structure of capsular polysaccharide biosynthesis genes in *Streptococcus agalactiae* Type Ia and Type Ib.

Please substitute the paragraph at page 10, lines 5-24 with the following replacement paragraph. A marked-up copy of this paragraph, showing the changes made thereto, is attached.

Also, in order to have the .beta 1,3-galactosyltransferase activity of the protein of the present invention, it has preferably at least 50% or more, preferably 60% or more, still more preferably 80% or more, most preferably 95% or more, of identity to the amino acid sequence represented by SEQ ID NO: 1. The identity of a nucleotide sequence or an amino acid sequence can be determined using the algorithm "BLAST" by Karlin and Altschl (*Proc. Natl. Acad. Sci. USA, 90*: 5873-5877 (1993)). The programs called "BLASTN" and "LASTX" have developed based on the above algorithm (*J. Mol. Biol., 215*: 403-410 (1990)). In the case of analyzing a nucleotide sequence based on BLAST, the parameter can be set to e.g. score = 100, wordlength = 12. And in the case of analyzing an amino acid sequence based on BLASTX, the parameter can be set to e.g. score = 50, wordlength = 3. In the case of using BLAST or Gapped BLAST program, a default